UNITED STATES PATENT AND TRADEMARK OFFICE

UNITED STATES DEPARTMENT OF COMMERCE
United States Patent and Trademark Office
Address: COMMISSIONER FOR PATENTS
P.O. Box 1450
Alexandria, Virginia 22313-1450
www.uspto.gov

APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/936,759	11/07/2001	Richard A. Jefferson	076518-0150	8995

39124 7590 02/16/2005

CAROL NOTTENBURG
814 32ND AVE 5
SEATTLE, WA 98144

EXAMINER	
VOGEL, NANCY S	
ART UNIT	**PAPER NUMBER**
1636	

DATE MAILED: 02/16/2005

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	09/936,759	JEFFERSON ET AL.	
	Examiner	Art Unit	
	Nancy T. Vogel	1636	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☐ Responsive to communication(s) filed on _____.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *36,37 and 60-63* is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *36,37 and 60-63* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☒ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☒ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☒ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☒ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) Paper No(s)/Mail Date *9/12/02, 4/26/02*.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____ .
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☒ Other: *seq. alignment*.

DETAILED ACTION

Claims 36, 37, and 60-63 are pending in the case.

Information Disclosure Statement

Receipt of Information disclosure statements on 9/12/02 and 4/26/02 is acknowledged. Certain citations have not been considered, since copies have not been received. These citations have been struck through and the information referred to therein has not been considered.

Drawings

New corrected drawings in compliance with 37 CFR 1.121(d) are required in this application because the text of some of the drawings cannot be read (Figures 5 and 5c). Applicant is advised to employ the services of a competent patent draftsperson outside the Office, as the U.S. Patent and Trademark Office no longer prepares new drawings. The corrected drawings are required in reply to the Office action to avoid abandonment of the application. The requirement for corrected drawings will not be held in abeyance.

Oath/Declaration

The oath or declaration is defective. A new oath or declaration in compliance with 37 CFR 1.67(a) identifying this application by application number and filing date is required. See MPEP §§ 602.01 and 602.02.

The oath or declaration is defective because:

It improperly lists a US patent application, 09/270,957, as a foreign application to which applicants claim benefit under 35 USC 119 (a-d).

Priority

It is noted that this application appears to claim subject matter disclosed in prior Application No. 09/270,957, filed 3/17/99. A reference to the prior application must be inserted as the first sentence of the specification of this application or in an application data sheet (37 CFR 1.76), if applicant intends to rely on the filing date of the prior application under 35 U.S.C. 119(e) or 120. See 37 CFR 1.78(a). For benefit claims under 35 U.S.C. 120, the reference must include the relationship (i.e., continuation, divisional, or continuation-in-part) of all nonprovisional applications. Also, the current status of all nonprovisional parent applications referenced should be included.

If the application is a utility or plant application filed under 35 U.S.C. 111(a) on or after November 29, 2000, the specific reference to the prior application must be submitted during the pendency of the application and within the later of four months from the actual filing date of the application or sixteen months from the filing date of the prior application. If the application is a utility or plant application which entered the national stage from an international application filed on or after November 29, 2000, after compliance with 35 U.S.C. 371, the specific reference must be submitted during the pendency of the application and within the later of four months from the date on which the national stage commenced under 35 U.S.C. 371(b) or (f) or sixteen months from the filing date of the prior application. See 37 CFR 1.78(a)(2)(ii) and (a)(5)(ii). This

time period is not extendable and a failure to submit the reference required by 35 U.S.C. 119(e) and/or 120, where applicable, within this time period is considered a waiver of any benefit of such prior application(s) under 35 U.S.C. 119(e), 120, 121 and 365(c). A priority claim filed after the required time period may be accepted if it is accompanied by a grantable petition to accept an unintentionally delayed claim for priority under 35 U.S.C. 119(e), 120, 121 and 365(c). The petition must be accompanied by (1) the reference required by 35 U.S.C. 120 or 119(e) and 37 CFR 1.78(a)(2) or (a)(5) to the prior application (unless previously submitted), (2) a surcharge under 37 CFR 1.17(t), and (3) a statement that the entire delay between the date the claim was due under 37 CFR 1.78(a)(2) or (a)(5) and the date the claim was filed was unintentional. The Director may require additional information where there is a question whether the delay was unintentional. The petition should be addressed to: Mail Stop Petition, Commissioner for Patents, P.O. Box 1450, Alexandria, Virginia 22313-1450.

Specification

The amendment filed 4/22/02 is objected to under 35 U.S.C. 132 because it introduces new matter into the disclosure. 35 U.S.C. 132 states that no amendment shall introduce new matter into the disclosure of the invention. The added material which is not supported by the original disclosure is as follows: the amendments to 49 which changes nucleotide sequences; a nucleotide sequence on page 56.

Applicant is required to cancel the new matter in the reply to this Office Action.

Double Patenting

A rejection based on double patenting of the "same invention" type finds its support in the language of 35 U.S.C. 101 which states that "whoever invents or discovers any new and useful process ... may obtain a patent therefor ..." (Emphasis added). Thus, the term "same invention," in this context, means an invention drawn to identical subject matter. See *Miller v. Eagle Mfg. Co.*, 151 U.S. 186 (1894); *In re Ockert*, 245 F.2d 467, 114 USPQ 330 (CCPA 1957); and *In re Vogel*, 422 F.2d 438, 164 USPQ 619 (CCPA 1970).

A statutory type (35 U.S.C. 101) double patenting rejection can be overcome by canceling or amending the conflicting claims so they are no longer coextensive in scope. The filing of a terminal disclaimer cannot overcome a double patenting rejection based upon 35 U.S.C. 101.

Claims 36 is provisionally rejected under 35 U.S.C. 101 as claiming the same invention as that of claim 36 of copending Application No. 10/364,649. This is a provisional double patenting rejection since the conflicting claim has not in fact been patented.

The nonstatutory double patenting rejection is based on a judicially created doctrine grounded in public policy (a policy reflected in the statute) so as to prevent the unjustified or improper timewise extension of the "right to exclude" granted by a patent and to prevent possible harassment by multiple assignees. See *In re Goodman*, 11 F.3d 1046, 29 USPQ2d 2010 (Fed. Cir. 1993); *In re Longi*, 759 F.2d 887, 225 USPQ 645 (Fed. Cir. 1985); *In re Van Ornum*, 686 F.2d 937, 214 USPQ 761 (CCPA 1982); *In re Vogel*, 422 F.2d 438, 164 USPQ 619 (CCPA 1970);and, *In re Thorington*, 418 F.2d 528, 163 USPQ 644 (CCPA 1969).

A timely filed terminal disclaimer in compliance with 37 CFR 1.321(c) may be used to overcome an actual or provisional rejection based on a nonstatutory double patenting ground provided the conflicting application or patent is shown to be commonly owned with this application. See 37 CFR 1.130(b).

Effective January 1, 1994, a registered attorney or agent of record may sign a terminal disclaimer. A terminal disclaimer signed by the assignee must fully comply with 37 CFR 3.73(b).

Claim 37 is provisionally rejected under the judicially created doctrine of obviousness-type double patenting as being unpatentable over claim 36 of copending Application No. 10/364,649. Although the conflicting claims are not identical, they are not patentably distinct from each other because the instant claim 37 recites beta glucuronidase which is encompassed by the beta-glucuronidases recited in copending 10/364,649, claim 36, since an isolated beta glucuronidase having 90% identity with the sequence shown in SEQ ID NO:6, would be encoded by a nucleic acid molecule that would hybridize under stringent conditions to the complement of nucleotides 1-1689 of SEQ ID NO:14.

This is a provisional obviousness-type double patenting rejection because the conflicting claims have not in fact been patented.

Claims 60-63 are provisionally rejected under the judicially created doctrine of obviousness-type double patenting as being unpatentable over claim 36 of copending Application No. 10/364,649 in view of Hochuli et al. (Bio/Technology 6:1321-1325, 1988)

Claim 36 of copending application 10/364,649 teaches an isolated beta-glucuronidase encoded by a nucleic acid molecule comprising nucleotides 1-1689 of Figure 4I-J (SEQ ID NO:14) or by a nucleic acid molecule that hybridizes under stringent conditions to the complement of said nucleic acid molecule. This nucleic acid molecule, and the beta-glucuronidase encoded by it, is the same as that disclosed in

Fig. 4I-J, or SEQ ID NO:14 of the instant application (nucleic acid) and SEQ ID NO:6 (protein).

The difference between the copending application and the instant claims is that the instant claims recite a fusion protein comprising the isolated beta-glucuronidase and a peptide, which may be hexa-His.

However, Hochuli et al. disclose protein fusions between a protein of interest, and a peptide of six histidine residues, i.e. "hexa-His", and the usefulness of said fusion protein for purification of the protein of interest (see . It would have been obvious to those of ordinary skill in the art, to have modified the protein which is the beta-glucuronidase of SEQ ID NO:14 in the US patent application 10/364,649, by fusing it to a peptide such as hexa-His, as taught by Hochuli et al., since the references generally concern the production and isolation of proteins of interest using genetic techniques, and since Hochuli et al. teach general techniques that are known in the art to be useful for isolation of proteins of interest or for bioassays. One would have been motivated to do so by the desire to obtain in purified form, the protein of interest which is disclosed by the US patent application, 10/364,649, since it is well known in the art that purified products have the advantage of lack of contaminants. Based upon the teachings of the cited references, the high skill of one of ordinary skill in the art, and absent evidence to the contrary, there would have been a reasonable expectation of success to result in the claimed invention.

This is a provisional obviousness-type double patenting rejection.

Claims 60-63 are provisionally rejected under the judicially created doctrine of obviousness-type double patenting as being unpatentable over claim 36 of copending Application No. 10/364,649 in view of Diamandis et al. (Clin. Chem. 37, 625, 1991) (cited by applicants).

Claim 36 of copending application 10/364,649 teaches an isolated beta-glucuronidase encoded by a nucleic acid molecule comprising nucleotides 1-1689 of Figure 4I-J (SEQ ID NO:14) or by a nucleic acid molecule that hybridizes under stringent conditions to the complement of said nucleic acid molecule. This nucleic acid molecule, and the beta-glucuronidase encoded by it, is the same as that disclosed in Fig. 4I-J, or SEQ ID NO:14 of the instant application (nucleic acid) and SEQ ID NO:6 (protein).

The difference between the copending application and the instant claims is that the instant claims recite a fusion protein comprising the isolated beta-glucuronidase and a peptide, which may be streptavidin.

However, Diamandis et al. teach fusion proteins between an enzyme of interest and streptavidin, and the usefulness of said fusion protein for such applications as immunoassays, flow cytometry, cell sorting, and Western blots (see Table 2 and pages 631-634). It would have been obvious to those of ordinary skill in the art, to have modified the protein which is the beta-glucuronidase of SEQ ID NO:14 in the US patent application 10/364,649, by fusing it to a peptide such as streptavidin, as taught by Diamandis et al., since the references concern enzymes of interest, and since Diamandis et al. teach general techniques of making enzyme- streptavidin fusions that

are known in the art to be applicable to enzymes whose activity is known, for use in biooassays. One would have been motivated to do so by the desire to obtain a beta-glucuronidase fusion useful for assays such as immunoassays. Based upon the teachings of the cited references, the high skill of one of ordinary skill in the art, and absent evidence to the contrary, there would have been a reasonable expectation of success to result in the claimed invention.

This is a provisional obviousness-type double patenting rejection.

Claim Rejections - 35 USC § 103

The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

> (a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

Claims 36, 37, and 60 are rejected under 35 U.S.C. 103(a) as being unpatentable over Nelson et al. (Nature, 399, 323-3329, 1999) in view of Jefferson et al. (GB 2 197 653, cited by applicants).

Nelson et al. disclose a beta-glucuronidase from Thermatoga maritima, which is encoded by a nucleic acid molecule comprising nucleotides 1-1689 of SEQ ID NO:14 of the instant application, or which comprises the amino acid sequence of SEQ ID NO:6 of the instant application (see attached sequence alignments). The difference between the reference and the instant application is that the beta-glucuronidase is isolated.

However, Jefferson et al. disclose the isolation of beta-glucuronidase from a bacteria (see pages 12, 16-17). It would have been obvious to one of ordinary skill in the art, to have isolated the beta-glucuronidase which is disclosed by Nelson et al. using such well known techniques as that disclosed by Jefferson for the isolation of beta-glucuronidase, since both references disclose beta-glucuronidases from bacteria and their sequences. One would have been motivated to do so by the well known usefulness of purified or isolated proteins, which are free of contaminants and thus in a useful form.

Claims 36, 37, 60-63 are rejected under 35 U.S.C. 103(a) as being unpatentable over Nelson et al. in view of Jefferson et al. as applied to claims 36 and 37 above, and further in view of Hochuli et al. (Bio/Technology 6:1321-1325, 1988).

Nelson et al. and Jefferson et al. are cited for the reasons set forth above.

The difference between the references and the instant claims is that the instant claims recite a fusion protein comprising the isolated beta-glucuronidase and a peptide, which may be hexa-His.

However, Hochuli et al. disclose protein fusions between a protein of interest, and a peptide of six histidine residues, i.e. "hexa-His", and the usefulness of said fusion protein for purification of the protein of interest (see . It would have been obvious to those of ordinary skill in the art, to have modified the protein which is the beta-glucuronidase taught by Nelson et al and Jefferson, by fusing it to a peptide such as hexa-His, as taught by Hochuli et al., since the references generally concern the

production and isolation of proteins of interest using genetic techniques, and since Hochuli et al. teach general techniques that are known in the art to be useful for isolation of proteins of interest or for bioassays. One would have been motivated to do so by the desire to obtain in purified form, the protein of interest which is disclosed by the US patent application, 10/364,649, since it is well known in the art that purified products have the advantage of lack of contaminants. Based upon the teachings of the cited references, the high skill of one of ordinary skill in the art, and absent evidence to the contrary, there would have been a reasonable expectation of success to result in the claimed invention.

Claims 36, 37, 60-63 are rejected under 35 U.S.C. 103(a) as being unpatentable over Nelson et al. in view of Jefferson et al. as applied to claims 36 and 37 above, and further in view of Diamandis et al. (Clin. Chem. 37, 625, 1991) (cited by applicants).

Nelson et al. and Jefferson et al. are cited for the reasons set forth above.

The difference between the copending application and the instant claims is that the instant claims recite a fusion protein comprising the isolated beta-glucuronidase and a peptide, which may be streptavidin.

However, Diamandis et al. teach fusion proteins between an enzyme of interest and streptavidin, and the usefulness of said fusion protein for such applications as immunoassays, flow cytometry, cell sorting, and Western blots (see Table 2 and pages 631-634). It would have been obvious to those of ordinary skill in the art, to have modified the protein which is the beta-glucuronidase as taught by Nelson et al. and

Jefferson, by fusing it to a peptide such as streptavidin, as taught by Diamandis et al., since the references concern enzymes of interest, and since Diamandis et al. teach general techniques of making enzyme- streptavidin fusions that are known in the art to be applicable to enzymes whose activity is known, for use in biooassays. One would have been motivated to do so by the desire to obtain a beta-glucuronidase fusion useful for assays such as immunoassays. Based upon the teachings of the cited references, the high skill of one of ordinary skill in the art, and absent evidence to the contrary, there would have been a reasonable expectation of success to result in the claimed invention.

Conclusion

No claims are allowed.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Nancy T. Vogel whose telephone number is (571) 272-0780. The examiner can normally be reached on 7:00 - 3:30, Monday - Friday.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Irem Yucel, Ph.D. can be reached on (571) 272-0781. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

Nancy T. Vogel, Ph.D.
Patent Examiner

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 24, 2005, 05:57:45 ; Search time 100 Seconds
(without alignments)
3239.359 Million cell updates/sec

Title: US-09-936-759-6
Perfect score: 3001
Sequence: 1 MVRPQRNKKRFILILNGVWN.....TRDRQPKLVAHVLRRLWSEV 563

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2999	99.9	563	2	Q9X0F2	Q9x0f2 thermotoga
2	1011	33.7	570	2	Q97UI1	Q97ui1 sulfolobus
3	977.5	32.6	599	2	Q8XP19	Q8xp19 clostridium
4	972.5	32.4	599	2	Q8VNV4	Q8vnv4 clostridium
5	929	31.0	602	2	Q9AFA2	Q9afa2 staphylococ
6	919.5	30.6	598	2	Q9AHJ8	Q9ahj8 lactobacill
7	906	30.2	670	2	Q6NL66	Q6nl66 drosophila
8	906	30.2	670	2	AAS93746	Aas93746 drosophil
9	905	30.2	656	2	Q9V8R0	Q9v8r0 drosophila
10	905	30.2	670	2	Q8MMB7	Q8mmb7 drosophila
11	902.5	30.1	648	1	BGLR_MOUSE	P12265 mus musculu
12	899.5	30.0	648	2	Q6IRI0	Q6ir10 mus musculu
13	898	29.9	651	1	BGLR_FELCA	O97524 felis silve
14	894.5	29.8	648	1	BGLR_RAT	P06760 rattus norv
15	888	29.6	651	1	BGLR_CANFA	O18835 canis famil
16	882	29.4	603	2	Q93VY4	Q93vy4 arabidopsis
17	880	29.3	603	2	Q8FHA3	Q8fha3 escherichia
18	879	29.3	603	1	BGLR_ECOLI	P05804 escherichia
19	879	29.3	603	2	Q9AHJ4	Q9ahj4 escherichia
20	872.5	29.1	648	1	BGLR_CERAE	O77695 cercopithec
21	865.5	28.8	651	1	BGLR_HUMAN	P08236 homo sapien
22	865.5	28.8	651	2	AAQ96851	Aaq96851 homo sapi
23	862	28.7	628	2	Q95Q32	Q95q32 caenorhabdi
24	861.5	28.7	603	2	Q6W7J7	Q6w7j7 ruminococcu
25	861.5	28.7	603	2	AAQ76046	Aaq76046 ruminococ
26	856.5	28.5	808	2	Q7TPJ3	Q7tpj3 rattus norv
27	841.5	28.0	686	2	Q9V9T9	Q9v9t9 drosophila
28	826.5	27.5	599	2	Q8E6A6	Q8e6a6 streptococc
29	821.5	27.4	599	2	Q8E0N2	Q8e0n2 streptococc
30	811	27.0	567	2	Q7UCE6	Q7uce6 shigella fl
31	809	27.0	567	2	Q83RC5	Q83rc5 shigella fl
32	728	24.3	660	2	Q7PZE2	Q7pze2 anopheles g
33	691	23.0	368	2	Q8X671	Q8x671 escherichia
34	691	23.0	370	2	Q7ADL5	Q7adl5 escherichia
35	531	17.7	459	2	Q8FMX0	Q8fmx0 corynebacte
36	487	16.2	755	2	Q92XF7	Q92xf7 rhizobium m
37	486.5	16.2	745	2	Q93IM0	Q93im0 thermoanaer
38	482	16.1	716	1	BGAL_THETU	P26257 thermoanaer
39	482	16.1	716	2	CAA38462	Caa38462 thermoana
40	481.5	16.0	998	1	BGAL_LACLA	Q48727 lactococcus
41	477.5	15.9	998	2	Q8VPU3	Q8vpu3 lactococcus
42	476.5	15.9	1085	2	O85250	O85250 thermotoga
43	472.5	15.7	996	2	O87523	O87523 lactococcus
44	460	15.3	743	1	BGAL_THEET	P77989 thermoanaer
45	452.5	15.1	1084	1	BGAL_THEMA	Q56307 thermotoga

ALIGNMENTS

RESULT 1
Q9X0F2
ID Q9X0F2 PRELIMINARY; PRT; 563 AA.
AC Q9X0F2;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Beta-glucuronidase.
GN OrderedLocusNames=TM1062;
OS Thermotoga maritima.
OC Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
OX NCBI_TaxID=2336;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MSB8 / DSM 3109 / ATCC 43589;
RX MEDLINE=99287316; PubMed=10360571; DOI=10.1038/20601;
RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
RA McDonald L.A., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.L.,
RA Heidelberg J.F., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT "Evidence for lateral gene transfer between Archaea and Bacteria from
RT genome sequence of Thermotoga maritima.";
RL Nature 399:323-329(1999).
DR EMBL; AE001766; AAD36143.1; -.
DR PIR; A72300; A72300.
DR HSSP; P08236; 1BHG.
DR TIGR; TM1062; -.
DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR008979; Gal_bind_like.
DR InterPro; IPR006101; Glyco_hydro_2.
DR InterPro; IPR006102; Glyco_hydro_2Ig.
DR InterPro; IPR006104; Glyco_hydro_2SB.
DR InterPro; IPR006103; Glyco_hydro_2TIM.
DR Pfam; PF00703; Glyco_hydro_2; 1.
DR Pfam; PF02836; Glyco_hydro_2_C; 1.
DR Pfam; PF02837; Glyco_hydro_2_N; 1.
DR PRINTS; PR00132; GLHYDRLASE2.
DR PROSITE; PS00719; GLYCOSYL_HYDROL_F2_1; 1.
KW Complete proteome.
SQ SEQUENCE 563 AA; 65682 MW; 98C030B75D33B6C1 CRC64;

Query Match 99.9%; Score 2999; DB 2; Length 563;
Best Local Similarity 99.8%; Pred. No. 4.1e-190;
Matches 562; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 MVRPQRNKKRFILILNGVWNLEVTSKDRPIAVPGSWNEQYQDLCYEEGPFTYKTTFYVPK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MVRPQRNKKRFILILNGVWNLEVTSKDRPIAVPGSWNEQYQDLCYEEGPFTYKTTFYVPK 60

Qy         61 XLSQKHIRLYFAAVNTDCEVFLNGEKVGENHIEYLPFEVDVTGKVKSGENELRVVVENRL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        61 ELSQKHIRLYFAAVNTDCEVFLNGEKVGENHIEYLPFEVDVTGKVKSGENELRVVVENRL 120

Qy       121 KVGGFPSKVPDSGTHTVGFFGSFPPANFDFFPYGGIIRPVLIEFTDHARILDIWVDTSES 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 KVGGFPSKVPDSGTHTVGFFGSFPPANFDFFPYGGIIRPVLIEFTDHARILDIWVDTSES 180

Qy       181 EPEKKLGKVKVKIEVSEEAVGQEMTIKLGEEEKKIRTSNRFVEGEFILENARFWSLEDPY 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 EPEKKLGKVKVKIEVSEEAVGQEMTIKLGEEEKKIRTSNRFVEGEFILENARFWSLEDPY 240

Qy       241 LYPLKVELEKDEYTLDIGIRTISWDEKRLYLNGKPVFLKGFGKHEEFPVLGQGTFYPLMI 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 LYPLKVELEKDEYTLDIGIRTISWDEKRLYLNGKPVFLKGFGKHEEFPVLGQGTFYPLMI 300

Qy       301 KDFNLLKKWINANSFRTSHYPYSEEWLDLADRLGILVIDEAPHVGITRYHYNPETQKIAED 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301 KDFNLLKKWINANSFRTSHYPYSEEWLDLADRLGILVIDEAPHVGITRYHYNPETQKIAED 360

Qy       361 NIRRMIDRHKNHPSVIMWSVANEPESNHPDAEGFFKALYETANEMDRTRPVVMVSMMDAP 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       361 NIRRMIDRHKNHPSVIMWSVANEPESNHPDAEGFFKALYETANEMDRTRPVVMVSMMDAP 420

Qy       421 DERTRDVALKYFDIVCVNRYYGWYIYQGRIEEGLQALEKDIEELYARHRKPIFVTEFGAD 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       421 DERTRDVALKYFDIVCVNRYYGWYIYQGRIEEGLQALEKDIEELYARHRKPIFVTEFGAD 480

Qy       481 AIAGIHYDPPQMFSEEYQAELVEKTIRLLLKKDYIIGTHVWAFADFKTPQNVRRPILNHK 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       481 AIAGIHYDPPQMFSEEYQAELVEKTIRLLLKKDYIIGTHVWAFADFKTPQNVRRPILNHK 540

Qy       541 GVFTRDRQPKLVAHVLRRLWSEV 563
            |||||||||||||||||||||||
Db       541 GVFTRDRQPKLVAHVLRRLWSEV 563
```

RESULT 2
Q97UI1
ID Q97UI1 PRELIMINARY; PRT; 570 AA.
AC Q97UI1;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Beta-glucuronidase (GusB) (EC 3.2.1.31).
GN Name=gusB; OrderedLocusNames=SSO3036;
OS Sulfolobus solfataricus.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=2287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 35092 / DSM 1617 / P2;
RX MEDLINE=21332296; PubMed=11427726;
RA She Q., Singh R.K., Confalonieri P., Zivanovic Y., Allard G.,
RA Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,
RA De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,
RA Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
RA Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
RA Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;
RT "The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
DR EMBL; AE006894; AAK43138.1; -.
DR PIR; C90485; C90485.
DR HSSP; P08236; 1BHG.
DR GO; GO:0004566; F:beta-glucuronidase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR008979; Gal_bind_like.
DR InterPro; IPR006101; Glyco_hydro_2.
DR InterPro; IPR006102; Glyco_hydro_2Ig.
DR InterPro; IPR006104; Glyco_hydro_2SB.
DR InterPro; IPR006103; Glyco_hydro_2TIM.
DR Pfam; PF00703; Glyco_hydro_2; 1.
DR Pfam; PF02836; Glyco_hydro_2_C; 1.
DR Pfam; PF02837; Glyco_hydro_2_N; 1.
DR PRINTS; PR00132; GLHYDRLASE2.
KW Complete proteome; Glycosidase; Hydrolase.
SQ SEQUENCE 570 AA; 66795 MW; DEB2FEC8050AF189 CRC64;

Query Match 33.7%; Score 1011; DB 2; Length 570;
Best Local Similarity 39.2%; Pred. No. 1.7e-58;
Matches 230; Conservative 92; Mismatches 191; Indels 74; Gaps 14;

```
Qy        15 LNGVWNLEVTSKDRP-------------IAVPGSWNEQYQDLCYEEGPFTYKTTFYVPK 60
             | | |  :: :::                | || |||||        |   |:   :|
Db        11 LQGFWKFKIDNENTGEENGWYKGLESEDIIYVPASWNEQNPKWDQFSGIAWYQKDLFVSN 70

Qy        61 XLSQKHIRLYFAAVNTDCEVFLNGEKVGENHIEYLPFEVDVTGKVKSGENELRVVVENRL 120
                :   : |        ::::|||  | :   :  |:  :  ||    ||   :|   :
Db        71 DNGNRKAWMVFEGAGYITKLWINGEYGGTHEGSFTQFKFPIKLKV----NEFNKIV---V 123

Qy       121 KVGGFPSKVPDSGTHTVGFFGSFPPAN------FDFFPYGGIIRPVLIEFTDHARILDIW 174
             |:   ||          : |||        |||| |||| ||| ||| |   : ||
Db       124 KIDNTPSPY-----------NLPPARDLNNAAFDFFNYGGIHRPVYIEFVDECHVEDIT 171

Qy       175 VDTSESEPEKKLGKVKVKIEVSEEAVGQEMTIKLGEEEKKI----RTSNRFVEGEFILEN 230
             | |       |  | :||:| :||      :  || ::| ::     :||    | :  : |
Db       172 VYT------KSYGHLKVEI-LSECNQRFSLRFKLVDKEGRVILNEEESSNEVFEKD--VNN 222

Qy       231 ARFWSLEDPYLYPLKVELE-----KDEYTLDIGIRTISWDEKRLYLNGKPVFLKGFGKHE 285
               || ::|||| | ||:      ||     || | :   : ::|||||:||||||:||
Db       223 VIPWSPDNPYLYTLIVEMYVGGNLKDSVYERIGFRDVEVKDGKIYLNGKPIFLKGFGRHE 282

Qy       286 EFPVLGQGTFYPLMIKDFNLLKWINANSFRTSHYPYSEEWLDLADRLGILVIDEAP--HV 343
             :||:||: |:  ::::|| |:: | |||||||||||| | ||||| :| ||| | |  :
Db       283 DFPILGKFTYGAVLVRDFYLMRKIGANSFRTSHYPYSNEHLDLADEMGFLVILEPPLCYS 342

Qy       344 GITRYHYNPETQKI---------AEDNIRRMIDRHKNHPSVIMWSVANEPESNHPDAEGF 394
               |:|     |  |:           | |: || :||| |||||:|| ||| |:  :   |
Db       343 NISRVMSQEEIAKMFGDVKYFEKVRDTIKEMIRQHKNRPSVIMYSVMNEPPSDIREVAEF 402

Qy       395 FKALYETANEMDRTRPVVMVSMMDAPDERTRDVALKYFDIVCVNRYYGWYIYQGRIEEGL 454
              :   |    :| :|||   |          ||:||:| |:: :| |:||   | |: |:
Db       403 IRREVELFKSLDSSRPVTFAS-----HRSVRDLALEYVDVISLNYYHGWYTEWGDIDSGV 457

Qy       455 QALEKDIEELYARH-RKPIFVTEFGADAIAGIHYDPPQMFSEEYQAELVEKTIRLLLKKD 513
             : :  ::||:: :   ||| :|||||||| |:| |||||:|||||:|:: | |  | :||
Db       458 KVVAIELEEIHKKFPEKPIIITEFGADAIYGLHSDPPQMWSEEYQSEMIRKYIEALREKD 517

Qy       514 YIIGTHVWAFADFKTPQNVRRPILNHKGVFTRDRQPKLVAHVLRRLW 560
             ||:| |:| ||||:||||  | ||| ||:|||||||| | |:  |:
Db       518 YIVGFHIWNFADFRTPQNPSRTILNRKGIFTRDRQPKLAAKVVEELF 564
```

RESULT 3
Q8XP19
ID Q8XP19 PRELIMINARY; PRT; 599 AA.
AC Q8XP19;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Beta-glucuronidase.
GN Name=bglR; OrderedLocusNames=CPE0147;
OS Clostridium perfringens.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1502;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=13;
RX MEDLINE=21664373; PubMed=11792842;
RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
RT "Complete genome sequence of Clostridium perfringens, an anaerobic
RT flesh-eater.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
DR EMBL; AP003185; BAB79853.1; -.

```
Db        241 TTCCTCAACGGAGAGAAAGTGGGAGAGAATCACATTGAATACCTTCCCTTCGAAGTAGAT 300
Qy        301 GTGACGGGGAAAGTGAAATCCGGAGAGAACGAACTCAGGGTGGTTGTTGAGAACAGATTG 360
Db        301 GTGACGGGGAAAGTGAAATCCGGAGAGAACGAACTCAGGGTGGTTGTTGAGAACAGATTG 360
Qy        361 AAAGTGGGAGGATTTCCCTCGAAGGTTCCAGACAGCGGCACTCACACCGTGGGATTTTTT 420
Db        361 AAAGTGGGAGGATTTCCCTCGAAGGTTCCAGACAGCGGCACTCACACCGTGGGATTTTTT 420
Qy        421 GGAAGTTTTCCACCTGCAAACTTCGACTTCTTCCCCTACGGTGGAATCATAAGGCCTGTT 480
Db        421 GGAAGTTTTCCACCTGCAAACTTCGACTTCTTCCCCTACGGTGGAATCATAAGGCCTGTT 480
Qy        481 CTGATAGAGTTCACAGACCACGCGAGGATACTCGACATCTGGGTGGACACGAGTGAGTCT 540
Db        481 CTGATAGAGTTCACAGACCACGCGAGGATACTCGACATCTGGGTGGACACGAGTGAGTCT 540
Qy        541 GAACCGGAGAAGAAACTTGGAAAAGTGAAAGTGAAGATAGAAGTCTCAGAAGAAGCGGTG 600
Db        541 GAACCGGAGAAGAAACTTGGAAAAGTGAAAGTGAAGATAGAAGTCTCAGAAGAAGCGGTG 600
Qy        601 GGACAGGAGATGACGATCAAACTTGGAGAGGAAGAGAAAAAGATTAGAACATCCAACAGA 660
Db        601 GGACAGGAGATGACGATCAAACTTGGAGAGGAAGAGAAAAAGATTAGAACATCCAACAGA 660
Qy        661 TTCGTCGAAGGGGAGTTCATCCTCGAAAACGCCAGGTTCTGGAGCCTCGAAGATCCATAT 720
Db        661 TTCGTCGAAGGGGAGTTCATCCTCGAAAACGCCAGGTTCTGGAGCCTCGAAGATCCATAT 720
Qy        721 CTTTATCCTCTCAAGGTGGAACTTGAAAAAGACGAGTACACTCTGGACATCGGAATCAGA 780
Db        721 CTTTATCCTCTCAAGGTGGAACTTGAAAAAGACGAGTACACTCTGGACATCGGAATCAGA 780
Qy        781 ACGATCAGCTGGGACGAGAAGAGGCTCTATCTGAACGGGAAACCTGTCTTTTTGAAGGGC 840
Db        781 ACGATCAGCTGGGACGAGAAGAGGCTCTATCTGAACGGGAAACCTGTCTTTTTGAAGGGC 840
Qy        841 TTTGGAAAGCACGAGGAATTCCCCGTTCTGGGGCAGGGCACCTTTTATCCATTGATGATA 900
Db        841 TTTGGAAAGCACGAGGAATTCCCCGTTCTGGGGCAGGGCACCTTTTATCCATTGATGATA 900
Qy        901 AAAGACTTCAACCTTCTGAAGTGGATCAACGCGAATTCTTTCAGGACCTCTCACTATCCT 960
Db        901 AAAGACTTCAACCTTCTGAAGTGGATCAACGCGAATTCTTTCAGGACCTCTCACTATCCT 960
Qy        961 TACAGTGAAGAGTGGCTGGATCTTGCCGACAGACTCGGAATCCTTGTGATAGACGAAGCC 1020
Db        961 TACAGTGAAGAGTGGCTGGATCTTGCCGACAGACTCGGAATCCTTGTGATAGACGAAGCC 1020
Qy       1021 CCGCACGTTGGTATCACAAGGTACCACTACAATCCCGAGACTCAGAAGATAGCAGAAGAC 1080
Db       1021 CCGCACGTTGGTATCACAAGGTACCACTACAATCCCGAGACTCAGAAGATAGCAGAAGAC 1080
Qy       1081 AACATAAGAAGAATGATCGACAGACACAAGAACCATCCCAGTGTGATCATGTGGAGTGTG 1140
Db       1081 AACATAAGAAGAATGATCGACAGACACAAGAACCATCCCAGTGTGATCATGTGGAGTGTG 1140
Qy       1141 GCGAACGAACCAGAGTCCAACCATCCAGACGCGGAGGGTTTCTTCAAAGCCCTTTATGAG 1200
Db       1141 GCGAACGAACCAGAGTCCAACCATCCAGACGCGGAGGGTTTCTTCAAAGCCCTTTATGAG 1200
Qy       1201 ACTGCCAATGAAATGGATCGAACACGCCCCGTTGTCATGGTGAGCATGATGGACGCACCA 1260
Db       1201 ACTGCCAATGAAATGGATCGAACACGCCCCGTTGTCATGGTGAGCATGATGGACGCACCA 1260
Qy       1261 GACGAGAGAACAAGAGACGTGGCGCTGAAGTACTTCGACATCGTCTGTGTGAACAGGTAC 1320
Db       1261 GACGAGAGAACAAGAGACGTGGCGCTGAAGTACTTCGACATCGTCTGTGTGAACAGGTAC 1320
Qy       1321 TACGGCTGGTACATCTATCAGGGAAGGATAGAAGAAGGACTTCAAGCTCTGGAAAAAGAC 1380
Db       1321 TACGGCTGGTACATCTATCAGGGAAGGATAGAAGAAGGACTTCAAGCTCTGGAAAAAGAC 1380
Qy       1381 ATAGAAGAGCTCTATGCAAGGCACAGAAAGCCCATCTTTGTCACAGAATTCGGTGCGGAC 1440
Db       1381 ATAGAAGAGCTCTATGCAAGGCACAGAAAGCCCATCTTTGTCACAGAATTCGGTGCGGAC 1440
Qy       1441 GCGATAGCTGGCATCCACTACGATCCACCTCAAATGTTCTCCGAAGAGTACCAAGCAGAG 1500
Db       1441 GCGATAGCTGGCATCCACTACGATCCACCTCAAATGTTCTCCGAAGAGTACCAAGCAGAG 1500
Qy       1501 CTCGTTGAAAAGACGATCAGGCTCCTTTTGAAAAAAGACTACATCATCGGAACACACGTG 1560
Db       1501 CTCGTTGAAAAGACGATCAGGCTCCTTTTGAAAAAAGACTACATCATCGGAACACACGTG 1560
Qy       1561 TGGGCCTTTGCAGATTTTAAGACTCCTCAGAATGTGAGAAGACCCATTCTCAACCACAAG 1620
Db       1561 TGGGCCTTTGCAGATTTTAAGACTCCTCAGAATGTGAGAAGACCCATTCTCAACCACAAG 1620
Qy       1621 GGTGTTTTCACAAGAGACAGACAACCCAAACTCGTTGCTCATGTACTGAGAAGACTGTGG 1680
Db       1621 GGTGTTTTCACAAGAGACAGACAACCCAAACTCGTTGCTCATGTACTGAGAAGACTGTGG 1680
Qy       1681 AGTGAGGTT 1689
Db       1681 AGTGAGGTT 1689
```

RESULT 2
AE001766/c

```
LOCUS       AE001766               12583 bp    DNA     linear   BCT 04-JUN-2004
DEFINITION  Thermotoga maritima MSB8 section 78 of 136 of the complete genome.
ACCESSION   AE001766 AE000512
VERSION     AE001766.1  GI:4981600
KEYWORDS    .
SOURCE      Thermotoga maritima MSB8
  ORGANISM  Thermotoga maritima MSB8
            Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
REFERENCE   1  (bases 1 to 12583)
  AUTHORS   Nelson,K.E., Clayton,R.A., Gill,S.R., Gwinn,M.L., Dodson,R.J.,
            Haft,D.H., Hickey,E.K., Peterson,J.D., Nelson,W.C., Ketchum,K.A.,
            McDonald,L., Utterback,T.R., Malek,J.A., Linher,K.D., Garrett,M.M.,
            Stewart,A.M., Cotton,M.D., Pratt,M.S., Phillips,C.A.,
            Richardson,D., Heidelberg,J., Sutton,G.G., Fleischmann,R.D.,
            Eisen,J.A., White,O., Salzberg,S.L., Smith,H.O., Venter,J.C. and
            Fraser,C.M.
  TITLE     Evidence for lateral gene transfer between Archaea and bacteria
            from genome sequence of Thermotoga maritima
  JOURNAL   Nature 399 (6734), 323-329 (1999)
  MEDLINE   99287316
   PUBMED   10360571
REFERENCE   2  (bases 1 to 12583)
  AUTHORS   Nelson,K.E., Clayton,R.A., Gill,S.R., Gwinn,M.L., Dodson,R.J.,
            Haft,D.H., Hickey,E.K., Peterson,J.D., Nelson,W.C., Ketchum,K.A.,
            McDonald,L., Utterback,T.R., Malek,J.A., Linher,K.D., Garrett,M.M.,
            Stewart,A.M., Cotton,M.D., Pratt,M.S., Phillips,C.A.,
            Richardson,D., Heidelberg,J., Sutton,G.G., Fleischmann,R.D.,
            White,O., Salzberg,S.L., Smith,H.O., Venter,J.C. and Fraser,C.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-JUN-1999) The Institute for Genomic Research, 9712
            Medical Center Dr, Rockville, MD 20850, USA
FEATURES             Location/Qualifiers
     source          1. .12583
                     /organism="Thermotoga maritima MSB8"
                     /mol_type="genomic DNA"
                     /strain="MSB8"
                     /db_xref="taxon:243274"
     gene            81. .1607
                     /locus_tag="TM1058"
     CDS             81. .1607
                     /locus_tag="TM1058"
                     /note="similar to GB:AE000666 percent identity: 48.70;
                     identified by sequence similarity; putative"
                     /codon_start=1
```

```
                     /transl_table=11
                     /product="glutamate synthase-related protein"
                     /protein_id="AAD36135.1"
                     /db_xref="GI:4981601"
                     /translation="MSGLCAKCVDGCTGGCETWLASFRGREVLYPGPFGDITAGAVKD
                     YPVDYSHLNILGYARGAEGLPEGVEPGPDTAIFTNVDTTTEYGWDIKVKMKVPIFTGA
                     LGSTEIARKNWDHIAVGAAISGITVVCGENVAGVDPDLELDSNGKVKKSPELDRRIEI
                     YKRYHDGEYGEILIQMNVEDTRLGVAEYVINKHGIETIELKWGQGAKSIGGEIKVRSL
                     ERALELKRRGYIVLPDPELPEVQRAFKEGEIKEFERHSRLGFVSKESFLKEVERLRKL
                     GFKRITLKTGAYSAVELAMALRYGAEAKVDLITVDGAPGGTGMSPWPMMNEWGIPTFY
                     LEALTYQFAEKLSRRGIRVPDIAIAGGFSTEDGVLKAIAMGSPYVKAVCMGRALMIPA
                     MVGKNIGEWLKSGNLPKTVSKYGTTVEEIFVTYEELRSRFGEEEVKKLPLGAIGVYTF
                     VQKFKTGLQQLMAGARKFRLSALSRKDLIALTKDAAEISGIPYVMESYRDEAERILEE
                     "
gene                 complement(1650. .1913)
                     /locus_tag="TM1059"
CDS                  complement(1650. .1913)
                     /locus_tag="TM1059"
                     /note="similar to SP:P45693 PID:862985 GB:AL009126 percent
                     identity: 48.70; identified by sequence similarity;
                     putative"
                     /codon_start=1
                     /transl_table=11
                     /product="spoVS-related protein"
                     /protein_id="AAD36136.1"
                     /db_xref="GI:4981602"
                     /translation="MEVLKVSSKSDPNKVAGAIAGVVREHGKAEIQAIGAGAVNQAVK
                     AIAIARGYLAPSGIDLVFVPAFTDVEIENEKRTAIKFIVFPKS"
gene                 complement(1962. .3272)
                     /locus_tag="TM1060"
CDS                  complement(1962. .3272)
                     /locus_tag="TM1060"
                     /note="similar to GB:AE000782 percent identity: 49.74;
                     identified by sequence similarity; putative"
                     /codon_start=1
                     /transl_table=11
                     /product="conserved hypothetical protein"
                     /protein_id="AAD36144.1"
                     /db_xref="GI:4981610"
                     /translation="MNISIIEGALAVLINQFFGGAYLTGYFLWMGASSFFIGLFGSIP
                     FLANTLQLLTLSFSHRLKSRKQIIVPLMWTARTSILLFAVFPAIKHGLLLAYLLYFYI
                     QIAGALSAPLWQSWMSDLVPKDMIGSYFGFRNLIHGAVQIPAMFLAGAILDSLGENWK
                     GFGTLFLIAGSLGALNGYFLKIQYEPPYKPREASVSITKAVKFLLKEEHFKNFLFGFA
                     FWNFAIGVGTVYINVMLLKEVEFSYLQISVLNAVGMFIGTLFQPFWGKLGDRYGFQYF
                     LKVCLWIHAIVILLWTLTPRSFLYVFFLQIIIGIFVTAGTSQLVFYTLMYTAPSSLKT
                     EAFSVFNSLSNLSLFAGSLVASVLVASLENISLPFGISAIRLTMFISFFLRASAAYII
                     SRMDLGTPQKVDSLIQAVKESFFSGTVPWIRERLNTLNIFRRKR"
gene                 complement(3382. .4545)
                     /locus_tag="TM1061"
CDS                  complement(3382. .4545)
                     /locus_tag="TM1061"
                     /note="similar to  percent identity: 0.00; identified by
                     sequence similarity; putative"
                     /codon_start=1
                     /transl_table=11
                     /product="hypothetical protein"
                     /protein_id="AAD36137.1"
                     /db_xref="GI:4981603"
                     /translation="MRSMTDVRRYWISLLRKICEMPLELCASDRLKKSMPVEGKKSEE
                     RRKFTHLELLGRIFCGISPFLELNRESPSTDPEERKIATRLSEFAVKSLDVATNPNCK
                     DYMNFKEGRQPLVDAAFLVEAILRAPKVLWEDLDVSTKKRLIRELKATRKIEPYFSNW
                     LLFSAMIETFFFFAGEEWDSTKVDLILKNVESWYKGDGAYGDGPFFRWDYYNSFVIYP
                     MTIDVLRIISEEKTEWKELYVKVLRRAQRYAVVLERMISPEGTFPIIGRSITYRTAVF
                     HLLSQLSLLHLLPASLSPAQVRCALTAVLRRIFENPSTFDENGWLKIGVIGSQPSLGE
                     EYITTGSLYLCTTVFLPLGLPTSDPFWRDPCKKWTNKKVWEGEDVAPDRALED"
gene                 complement(4542. .6233)
                     /locus_tag="TM1062"
CDS                  complement(4542. .6233)
                     /locus_tag="TM1062"
                     /note="similar to PID:642973 PID:14446 PID:412358 percent
                     identity: 57.73; identified by sequence similarity;
                     putative"
                     /codon_start=1
                     /transl_table=11
                     /product="beta-glucuronidase"
                     /protein_id="AAD36143.1"
                     /db_xref="GI:4981609"
                     /translation="MVRPQRNKKRFILILNGVWNLEVTSKDRPIAVPGSWNEQYQDLC
                     YEEGPFTYKTTFYVPKELSQKHIRLYFAAVNTDCEVFLNGEKVGENHIEYLPFEVDVT
                     GKVKSGENELRVVVENRLKVGGFPSKVPDSGTHTVGFFGSFPPANFDFFPYGGIIRPV
                     LIEFTDHARILDIWVDTSESEPEKKLGKVKVKIEVSEEAVGQEMTIKLGEEEKKIRTS
                     NRFVEGEFILENARFWSLEDPYLYPLKVELEKDEYTLDIGIRTISWDEKRLYLNGKPV
                     FLKGFGKHEEFPVLGQGTFYPLMIKDFNLLKWINANSFRTSHYPYSEEWLDLADRLGI
                     LVIDEAPHVGITRYHYNPETQKIAEDNIRRMIDRHKNHPSVIMWSVANEPESNHPDAE
                     GFFKALYETANEMDRTRPVVMVSMMDAPDERTRDVALKYFDIVCVNRYYGWYIYQGRI
                     EEGLQALEKDIEELYARHRKPIFVTEFGADAIAGIHYDPPQMFSEEYQAELVEKTIRL
                     LLKKDYIIGTHVWAFADFKTPQNVRRPILNHKGVFTRDRQPKLVAHVLRRLWSEV"
gene                 complement(6284. .7309)
                     /locus_tag="TM1063"
CDS                  complement(6284. .7309)
                     /locus_tag="TM1063"
                     /note="similar to SP:P42065 PID:677944 GB:AL009126 percent
                     identity: 75.31; identified by sequence similarity;
                     putative"
                     /codon_start=1
                     /transl_table=11
                     /product="oligopeptide ABC transporter, ATP-binding
                     protein"
                     /protein_id="AAD36138.1"
                     /db_xref="GI:4981604"
                     /translation="MALLEVKNLKKYFPIIKRGFRRKVVGYLKAVDGISFHIEEGETL
                     GLVGESGCGKTTTAKLIMRGIEPTEGEIVLNMDGEKVDITKLSEKELREKGVRRFLQM
                     IFQDPYSSLNPRMTVRDIIAEPLVVNGVIKGKEEIDAIVSDLLRAVGLRPEYMQRYPH
                     AFSGGQRQRIAIARAIALKPKLVLCDEPTSALDVSVQAQIINLLKDLQKEYNLTYLFI
                     SHDLGVVEHITNRVAVMYVGRIVELAETEELFSSPKHPYTEALLSAVPKPDPKRKRKK
                     AQLTGEVPDPSNPPSGCYFHPRCPYAKAICKEVYPDLRNVGTDQNPHLVACHFADSLK
                     LEGVGTM"
gene                 complement(7296. .8294)
                     /locus_tag="TM1064"
CDS                  complement(7296. .8294)
                     /locus_tag="TM1064"
                     /note="similar to SP:P42064 PID:677943 GB:AL009126 percent
                     identity: 72.95; identified by sequence similarity;
                     putative"
                     /codon_start=1
                     /transl_table=11
                     /product="oligopeptide ABC transporter, ATP-binding
                     protein"
                     /protein_id="AAD36139.1"
                     /db_xref="GI:4981605"
                     /translation="MSTLLQIKNLRTYFFTDEGVVKAVDGVSFEIEEGRTLGVVGESG
                     CGKSVTARSIIKLLSTAGRIVSGEILYNMDGQMVDLVKFSKEEIRKVRGRHIAMIFQE
                     PMAAFSPVYTIGDQITEGMIYHFGITKQEARERAVELLRRVGIPKPEKMIDSYPFEYS
                     GGMRQRAMIAMALSCNPRLLIADEPTTALDVTIQAQVLDLLKDLQQEYKMAIMMITHN
                     MGVVAEMADHVVVMYLGRVVESAPVEELFYNPKHPYTSLLLRSIPVVGKRVERLEVIE
                     GDVPDPRNMPKGCRFHPRCPYMMKGICDEREPVEVEVGPEHRVSCFLYGGEKDGAS"
gene                 complement(8306. .9409)
                     /locus_tag="TM1065"
CDS                  complement(8306. .9409)
                     /locus_tag="TM1065"
                     /note="similar to GB:AE000657 percent identity: 67.80;
                     identified by sequence similarity; putative"
                     /codon_start=1
                     /transl_table=11
                     /product="oligopeptide ABC transporter, permease protein"
                     /protein_id="AAD36140.1"
                     /db_xref="GI:4981606"
                     /translation="MKKREQMEEKFYYASQWQLIWWRFRKHKLAVIGGVVLLIIYVFA
                     IFCEFFAPYDPNKYNYRYPYAPPQRIHFFHEGKFIGPFVYGYTYTVDLETLRRIYKED
                     KSKIFKIKFFVRGDEYKFWGIWKTNIHFIGVEDGHMFLLGTDSLGRDMLSRIIYGARI
                     STSIGLIGVFLSFILGVAIGGISGYFGGAVDNFIQRTIEIIKSIPTIPLWLALSAALP
                     QNWPPLRVYFVIVIILSLTGWTDLARVVRSRFLSLREEDFVMAAKFMGASEARIIFRH
                     MLPSFMSHLIASITLSIPGMILGETSLSFLGLGLRPPVISWGVLLQEAQNLTVVALYP
                     WLLIPVVFVITTVLCFNFVGDGLRDAADPYANM"
gene                 complement(9420. .10403)
                     /locus_tag="TM1066"
```

```
     CDS             complement(9420. .10403)
                     /locus_tag="TM1066"
                     /note="similar to SP:P42062 PID:677946 GB:AL009126 percent
                     identity: 62.93; identified by sequence similarity;
                     putative"
                     /codon_start=1
                     /transl_table=11
                     /product="oligopeptide ABC transporter, permease protein"
                     /protein_id="AAD36141.1"
                     /db_xref="GI:4981607"

  Query Match             99.9%;  Score 1688;  DB 1;  Length 12583;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1688;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATGGTAAGACCGCAACGAAACAAGAAGAGATTTATTCTTATCTTGAATGGAGTTTGGAAT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6233 ATGGTAAGACCGCAACGAAACAAGAAGAGATTTATTCTTATCTTGAATGGAGTTTGGAAT 6174

Qy         61 CTTGAAGTAACCAGCAAAGACAGACCAATCGCCGTTCCTGGAAGCTGGAATGAGCAGTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6173 CTTGAAGTAACCAGCAAAGACAGACCAATCGCCGTTCCTGGAAGCTGGAATGAGCAGTAC 6114

Qy        121 CAGGATCTGTGCTACGAAGAAGGACCCTTCACCTACAAAACCACCTTCTACGTTCCGAAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6113 CAGGATCTGTGCTACGAAGAAGGACCCTTCACCTACAAAACCACCTTCTACGTTCCGAAG 6054

Qy        181 NAACTTTCACAAAAACACATCAGACTTTACTTTGCTGCGGTGAACACGGACTGCGAGGTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6053 GAACTTTCACAAAAACACATCAGACTTTACTTTGCTGCGGTGAACACGGACTGCGAGGTC 5994

Qy        241 TTCCTCAACGGAGAGAAAGTGGGAGAGAATCACATTGAATACCTTCCCTTCGAAGTAGAT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5993 TTCCTCAACGGAGAGAAAGTGGGAGAGAATCACATTGAATACCTTCCCTTCGAAGTAGAT 5934

Qy        301 GTGACGGGGAAAGTGAAATCCGGAGAGAACGAACTCAGGGTGGTTGTTGAGAACAGATTG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5933 GTGACGGGGAAAGTGAAATCCGGAGAGAACGAACTCAGGGTGGTTGTTGAGAACAGATTG 5874

Qy        361 AAAGTGGGAGGATTTCCCTCGAAGGTTCCAGACAGCGGCACTCACACCGTGGGATTTTTT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5873 AAAGTGGGAGGATTTCCCTCGAAGGTTCCAGACAGCGGCACTCACACCGTGGGATTTTTT 5814

Qy        421 GGAAGTTTTCCACCTGCAAACTTCGACTTCTTCCCCTACGGTGGAATCATAAGGCCTGTT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5813 GGAAGTTTTCCACCTGCAAACTTCGACTTCTTCCCCTACGGTGGAATCATAAGGCCTGTT 5754

Qy        481 CTGATAGAGTTCACAGACCACGCGAGGATACTCGACATCTGGGTGGACACGAGTGAGTCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5753 CTGATAGAGTTCACAGACCACGCGAGGATACTCGACATCTGGGTGGACACGAGTGAGTCT 5694

Qy        541 GAACCGGAGAAGAAACTTGGAAAAGTGAAAGTGAAGATAGAAGTCTCAGAAGAAGCGGTG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5693 GAACCGGAGAAGAAACTTGGAAAAGTGAAAGTGAAGATAGAAGTCTCAGAAGAAGCGGTG 5634

Qy        601 GGACAGGAGATGACGATCAAACTTGGAGAGGAAGAGAAAAAGATTAGAACATCCAACAGA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5633 GGACAGGAGATGACGATCAAACTTGGAGAGGAAGAGAAAAAGATTAGAACATCCAACAGA 5574

Qy        661 TTCGTCGAAGGGGAGTTCATCCTCGAAAACGCCAGGTTCTGGAGCCTCGAAGATCCATAT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5573 TTCGTCGAAGGGGAGTTCATCCTCGAAAACGCCAGGTTCTGGAGCCTCGAAGATCCATAT 5514

Qy        721 CTTTATCCTCTCAAGGTGGAACTTGAAAAAGACGAGTACACTCTGGACATCGGAATCAGA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5513 CTTTATCCTCTCAAGGTGGAACTTGAAAAAGACGAGTACACTCTGGACATCGGAATCAGA 5454

Qy        781 ACGATCAGCTGGGACGAGAAGAGGCTCTATCTGAACGGGAAACCTGTCTTTTTGAAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5453 ACGATCAGCTGGGACGAGAAGAGGCTCTATCTGAACGGGAAACCTGTCTTTTTGAAGGGC 5394

Qy        841 TTTGGAAAGCACGAGGAATTCCCCGTTCTGGGGCAGGGCACCTTTTATCCATTGATGATA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db       5393 TTTGGAAAGCACGAGGAATTCCCCGTTCTGGGGCAGGGCACCTTTTATCCATTGATGATA 5334

Qy         901 AAAGACTTCAACCTTCTGAAGTGGATCAACGCGAATTCTTTCAGGACCTCTCACTATCCT 960
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5333 AAAGACTTCAACCTTCTGAAGTGGATCAACGCGAATTCTTTCAGGACCTCTCACTATCCT 5274

Qy         961 TACAGTGAAGAGTGGCTGGATCTTGCCGACAGACTCGGAATCCTTGTGATAGACGAAGCC 1020
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5273 TACAGTGAAGAGTGGCTGGATCTTGCCGACAGACTCGGAATCCTTGTGATAGACGAAGCC 5214

Qy        1021 CCGCACGTTGGTATCACAAGGTACCACTACAATCCCGAGACTCAGAAGATAGCAGAAGAC 1080
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5213 CCGCACGTTGGTATCACAAGGTACCACTACAATCCCGAGACTCAGAAGATAGCAGAAGAC 5154

Qy        1081 AACATAAGAAGAATGATCGACAGACACAAGAACCATCCCAGTGTGATCATGTGGAGTGTG 1140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5153 AACATAAGAAGAATGATCGACAGACACAAGAACCATCCCAGTGTGATCATGTGGAGTGTG 5094

Qy        1141 GCGAACGAACCAGAGTCCAACCATCCAGACGCGGAGGGTTTCTTCAAAGCCCTTTATGAG 1200
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5093 GCGAACGAACCAGAGTCCAACCATCCAGACGCGGAGGGTTTCTTCAAAGCCCTTTATGAG 5034

Qy        1201 ACTGCCAATGAAATGGATCGAACACGCCCCGTTGTCATGGTGAGCATGATGGACGCACCA 1260
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5033 ACTGCCAATGAAATGGATCGAACACGCCCCGTTGTCATGGTGAGCATGATGGACGCACCA 4974

Qy        1261 GACGAGAGAACAAGAGACGTGGCGCTGAAGTACTTCGACATCGTCTGTGTGAACAGGTAC 1320
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4973 GACGAGAGAACAAGAGACGTGGCGCTGAAGTACTTCGACATCGTCTGTGTGAACAGGTAC 4914

Qy        1321 TACGGCTGGTACATCTATCAGGGAAGGATAGAAGAAGGACTTCAAGCTCTGGAAAAAGAC 1380
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4913 TACGGCTGGTACATCTATCAGGGAAGGATAGAAGAAGGACTTCAAGCTCTGGAAAAAGAC 4854

Qy        1381 ATAGAAGAGCTCTATGCAAGGCACAGAAAGCCCATCTTTGTCACAGAATTCGGTGCGGAC 1440
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4853 ATAGAAGAGCTCTATGCAAGGCACAGAAAGCCCATCTTTGTCACAGAATTCGGTGCGGAC 4794

Qy        1441 GCGATAGCTGGCATCCACTACGATCCACCTCAAATGTTCTCCGAAGAGTACCAAGCAGAG 1500
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4793 GCGATAGCTGGCATCCACTACGATCCACCTCAAATGTTCTCCGAAGAGTACCAAGCAGAG 4734

Qy        1501 CTCGTTGAAAAGACGATCAGGCTCCTTTTGAAAAAAGACTACATCATCGGAACACACGTG 1560
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4733 CTCGTTGAAAAGACGATCAGGCTCCTTTTGAAAAAAGACTACATCATCGGAACACACGTG 4674

Qy        1561 TGGGCCTTTGCAGATTTTAAGACTCCTCAGAATGTGAGAAGACCCATTCTCAACCACAAG 1620
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4673 TGGGCCTTTGCAGATTTTAAGACTCCTCAGAATGTGAGAAGACCCATTCTCAACCACAAG 4614

Qy        1621 GGTGTTTTCACAAGAGACAGACAACCCAAACTCGTTGCTCATGTACTGAGAAGACTGTGG 1680
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4613 GGTGTTTTCACAAGAGACAGACAACCCAAACTCGTTGCTCATGTACTGAGAAGACTGTGG 4554

Qy        1681 AGTGAGGTT 1689
               |||||||||
Db       4553 AGTGAGGTT 4545


RESULT 3
AF012423
LOCUS       AF012423               2153 bp    mRNA    linear   MAM 09-SEP-1999
DEFINITION  Felis catus beta-glucuronidase (GUSB) mRNA, complete cds.
ACCESSION   AF012423
VERSION     AF012423.1  GI:4102550
KEYWORDS    .
SOURCE      Felis catus (cat)
  ORGANISM  Felis catus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
REFERENCE   1  (bases 1 to 2153)
  AUTHORS   Fyfe,J.C., Kurzhals,R.L., Lassaline,M.E., Henthorn,P.S., Alur,P.R.,
            Wang,P., Wolfe,J.H., Giger,U., Haskins,M.E., Patterson,D.F.,
```